REMARKS

Reconsideration and reexamination of the subject application are respectfully requested in light of the foregoing amendments and following remarks. The amendments are made without prejudice or disclaimer of Applicants' right to claim any subject matter disclosed in the specification in a subsequently filed continuing application.

1. Status of the Claims

Claims 1-10 are pending. Claims 1-10 stand rejected. Claim 11 is added by the present amendment.

2. Support for the Amendments

The amendments to claim 1 include substitution of the term "an" with the term "the," which is added to clarify the nature of the invention. "SEQ. ID. No." is replaced with "SEQ ID NO" to comport with U.S. practice. The amendments further clarify that the protein and nucleic acid of claims 1 and 2, respectively, are "isolated." Support for an isolated protein and nucleic acid is found throughout the specification, e.g., page 11, line 25 through page 12, line 27.

Claim 1 is further amended to replace a gene of SEQ ID NO: 2 with a polynucleotide that encodes the protein of SEQ ID NO: 1. Support for the amendment is found, for example, at page 4, lines 7-8; page 7, line 11 (encoding gene); and page 10, line 9, *et seq*. (encoding RNA). The Office is further respectfully directed to the Federal Circuit's holding in *In re Wallach*, 378 F.3d 1330, 71 U.S.P.Q.2d 1939 (Fed. Cir. 2004). The Court held that the state of the art has developed such that the complete amino acid sequence of a protein may put one in possession of the genus of DNA sequences encoding it, and that one of ordinary skill in the art would be in possession of the entire genus of DNA sequences that can encode even a partially disclosed protein sequence, even if the individual species within that genus might not have been described. *Wallach*, 71 U.S.P.Q.2d at 1942 (citing with approval M.P.E.P. § 2163(II)(A)(3)(a)(ii), 8th ed., revised February 2001). The description of the protein of SEQ ID NO: 1 puts the artisan in

possession of a genus of nucleic acids encoding the protein of SEQ ID NO: 1, which includes the nucleic acid of SEQ ID NO: 2. *See Wallach*, 71 U.S.P.Q.2d at 1942.

3. Notice of Prosecution in a Co-Pending Application

Applicants bring to the Office's attention prosecution in co-pending Application Serial No 10/588,140 ("the '140 application"), titled "Protein with activity of hydrolyzing dextran, starch, mutan, inulin and levan, gene encoding the same, cell expressing the same, and production method." A non-final Office Action was mailed in the '140 application on December 28, 2007. The Office Action cites U.S. Patent No. 6,485,953 ("Kim") and U.S. Patent No. 5,637,491 in rejections under 35 U.S.C. § 102(b). The Office Action also cites Kim in view of Standing, *Curr. Opinion Struct. Biol.* 13(5): 595-601 (2003); Sambrook *et al.* **In** MOLECULAR CLONING: A LABORATORY MANUAL, 2nd ed., Cold Spring Harbor, N.Y., pp 8.46-8.52 and 11.2-11.19 (1989); and U.S. Patent No. 5,643,758 in rejections under 35 U.S.C. § 103.

4. Acceptance of Drawings

Applicants note with appreciation the indication that all the drawings filed on July 31, 2006, are accepted.

5. Acknowledgement of Certified Priority Documents

Applicants note with appreciation the indication that all of the certified priority documents have been received in this matter.

6. Acknowledgement of Information Disclosure Statement

Applicants note with appreciation the acknowledgement of the Information Disclosure Statements filed July 31, 2006, February 13, 2007, and September 7, 2007.

7. Rejection under 35 U.S.C. § 101

Claims 1 and 2 are rejected under 35 U.S.C. § 101 as allegedly directed to non-statutory subject matter. The claims are amended to indicate that the protein and nucleic acid are

"isolated," i.e., are products of the hand of man. The claims are directed to statutory subject matter. *Diamond v. Chakrabarty*, 447 U.S. 303 (1980). Accordingly, the rejection should be withdrawn.

8. Rejection under 35 U.S.C. § 112, Second Paragraph

Claim 5 is rejected under 35 U.S.C. § 112, second paragraph, because it is allegedly unclear whether Accession No. KCTC 10573BP is *E. coli* BL21(DE3)pLysS transformed with pRSET-LSA. The Office requires Applicants to confirm whether the deposited organism contains a nucleic acid having the sequence of SEQ ID NO: 2. Applicants traverse the rejection.

The specification at page 7, lines 21-27, discloses that the microorganism deposited as Accession No. KCTC 10573BP is *Escherichia coli* DH5@/pRLSA. The same information also is provided in the Receipt in the Case of an Original Deposit, a copy of which is attached as **Exhibit 1**. From the specification, page 12, lines 13-16, it is clear that *E. coli* DH5@/pRLSA is transformed with pRSET-LSA, which contains the *lsa* gene inserted into a SacI-EcoRI site of a pRSETB vector (Invitrogen USA). The *lsa* gene is disclosed in Figure 1. *See, e.g.*, Specification, page 16, line 13, *et seq.* The polynucleotide disclosed in Figure 1 has the sequence of SEQ ID NO: 2 and encodes a protein having the amino acid sequence of SEQ ID NO: 1. *See* Figure 1; Sequence Listing, e.g., line 223: "*Escherichia coli* DH5@/pRLSA." Accordingly, the nature of the deposited organism is clear from the specification. For instance, it is clear that the deposited organism contains the nucleic acid of SEQ ID NO: 2, which encodes the protein of SEQ ID NO: 1. The rejection thus should be withdrawn.

9. Rejection under 35 U.S.C. § 112, First Paragraph (Enablement)

Claims 1-4 and 6-10 are rejected under 35 U.S.C. § 112, first paragraph, as allegedly directed to subject matter requiring undue experimentation to make or use. Applicants traverse the rejection.

The Office acknowledges that the specification enables the subject matter of an isolated protein comprising the amino acid sequence of SEQ ID NO: 1, which has the activity of hydrolyzing amylopectin, starch, glycogen, and amylase. To expedite prosecution, claim 1 is

amended to recite what the Office acknowledges as enabled, and this aspect of the rejection accordingly should be withdrawn.

The Office further acknowledges that an isolated polynucleotide comprising the nucleotide sequence of SEQ ID NO: 2 is enabled. New claim 11 is directed to this subject matter.

Amended claim 2 recites an isolated polynucleotide encoding the protein of claim 1, i.e., the protein comprising the amino acid sequence of SEQ ID NO: 1. It was well known in the art at the time of the invention that multiple polynucleotide sequences can encode a particular amino acid sequence, given the know redundancy of the genetic code. *See, e.g.*, *Wallace*, 71 U.S.P.Q.2d at 1942 (referring to MOLECULAR BIOLOGY OF THE GENE, Watson *et al.*, eds., Benjamin/Cummings, 3rd ed., pp. 356-57 (1977) for the proposition that the skilled artisan would know every combination of sequences of a polynucleotide that would encode a particular polypeptide). The artisan also knew how to construct polynucleotide sequences having any combination of nucleotide bases by routine synthetic chemistry, for example. *See, e.g.*, Sambrook *et al.* **In** MOLECULAR CLONING: A LABORATORY MANUAL, 2nd ed., Cold Spring Harbor, N.Y., p. 8.49 (1989). Although a significant amount of experimentation would be required to make all polynucleotide sequences encompassed by the claim, the experimentation itself was routine and predictable, given this level of skill in the art. For these reasons, the experimentation would not be undue in nature. *See In re Wands*, 858 F.2d 731, 736, 8 U.S.P.Q.2d 1400, 1404 (Fed. Cir. 1988); *Johns Hopkins Univ. v. Cellpro, Inc.*, 152 F.3d 1342, 1360, 47 U.S.P.Q.2d 1705, 1719 (Fed. Cir. 1998) ("the test [for undue experimentation] is not merely quantitative . . . if it is merely routine"). Because the experimentation required to make and use the claimed invention is not undue, claim 2 is enabled by the specification. Because the polynucleotide of claim 2 is enabled, the subject matter of the dependent claims 3-10 also is enabled. The rejection accordingly should be withdrawn.

10. <u>Rejection under 35 U.S.C. § 112, First Paragraph (Biological Deposit)</u>

Claim 5 is rejected as allegedly non-enabled, because the specification does not indicate whether the deposited microorganism will be available to the public. As shown in **Exhibit 1**, for

example, the deposited microorganism having Accession No. KCTC 10573BP was deposited under the terms of the Budapest Treaty. The undersigned attorney of record states that the deposited microorganism having Accession No. KCTC 10573BP will be released to the public irrevocably and without restriction or condition upon issuance of a patent. Applicants have satisfied the deposit requirements, and the rejection should be withdrawn.

11. Rejection under 35 U.S.C. § 112, First Paragraph (Written Description)

Claims 1-4 are rejected under 35 U.S.C. § 112, first paragraph, as allegedly inadequately described in the specification. Applicants traverse the rejection.

The protein of claim 1 is adequately described by the amino acid sequence of SEQ ID NO: 1, and the polynucleotide of claim 11 is adequately described by the nucleotide sequence of SEQ ID NO: 2. The polynucleotide of claim 2 is adequately described for the reasons set forth at Part 2, above. That is, the Office's reviewing court has held that the state of the art has developed such that a description of a complete amino acid sequence of a protein puts the artisan in possession of a genus of DNA sequences encoding it. *See Wallach*, 71 U.S.P.Q.2d at 1942. It follows that the description of the protein of SEQ ID NO: 1 puts the artisan in possession of a genus of nucleic acids encoding the protein of SEQ ID NO: 1. *See Id.* Because the polynucleotide of claim 2 is described, the transformed cell of claims 3 and 4 likewise is adequately described. The rejection accordingly should be withdrawn.

12. Rejections under 35 U.S.C. § 102

U.S. Patent No. 6,485,953 ("Kim")

Claims 1 and 7-10 are rejected under 35 U.S.C. § 102(b) as allegedly anticipated by U.S. Patent No. 6,485,953 ("Kim"). Applicants traverse the rejection.

To establish a *prima facie* case of anticipation, a single prior art reference must teach each and every element of the claimed invention, either explicitly or inherently. *Verdegaal Bros. v. Union Oil Co. Cal.*, 814 F.2d 628, 631, 2 U.S.P.Q.2d 1051, 1053 (Fed. Cir. 1987). Recognizing that the Office does not possess means to test inherent characteristics

experimentally, the Office's reviewing courts require the Office only to establish a reason to believe that a property is an inherent characteristic of the prior art. *In re Best*, 562 F.2d 1252, 195 U.S.P.Q. 430, 433 (C.C.P.A. 1977). The Office must establish further that the allegedly inherent characteristic ***necessarily*** inheres in the prior art teaching. *See, e.g., In re Oelrich*, 666 F.2d 578, 581-82 (C.C.P.A. 1981) ("Inherency, however, may not be established by probabilities or possibilities.").

In the present case, the Office has not put forth adequate reasons or evidence that the protein disclosed in Kim is the same as the presently claimed protein. Like the claimed protein, the protein disclosed in Kim is a dextranase and amylase secreted from *L. starkeyi*. *L. starkeyi*, however, secretes a battery of dextranases, amylases, and other glucanhydrolases. *See* Kang *et al.*, "Cloning and expression of *Lipomyces starkeyi* α-amylase in *Escherichia coli* and determination of some of its properties," *FEMS Microbiol. Lett.* 233: 53-64 (2004), page 62, right col. (citing references). The Office has established only a mere ***possibility*** that the Kim protein is indeed the protein of SEQ ID NO: 1 and not another of the battery of secreted proteins. This evidence is insufficient to make a case of inherent anticipation. *See Oelrich*, 666 F.2d at 581-82.

Further, there are differences in the properties of the protein of SEQ ID NO: 1 and the protein of Kim. For instance, [1] the apparent molecular weight is different between the two *L. starkeyi* enzymes. The protein of Kim exhibits an apparent molecular weight using 10% SDS-PAGE of 94 kDa and 60 kDa. Kim, col. 2, lines 41-46. The native protein of SEQ ID NO: 1 has an apparent molecular weight of 100 kDa, and the expressed protein (fused with a His-tag) has an apparent molecular weight of 73 kDa in a Western blot. E.g., Specification, page 19, line 8, and page 20, line 4.

[2] The pH optima for the enzymes also are distinct. The protein of Kim shows an optimal pH for dextranase activity of pH 3.5-5.5 (Figure 1A) and an optimal pH for amylase activity of pH 3.5-4.5 (Figure 1B). For both dextranse and amylase activities, nearly half of the activity is lost at a pH of 7.5 or 5.5, respectively. By contrast, the protein of SEQ ID NO: 1 shows a broad pH dependence for carbohydrolase activity (*see* Specification, page 14, line 11, *et*

seq.). As shown in the specification at Figure 5, the presently disclosed protein retains nearly full activity at pH 8.

[3] The enzymes display further differences in their dependence on cations. The protein of Kim displays 100% activity in 10 mM EDTA. *See* Kim, Table 2. By contrast, the presently disclosed protein displays only 46% activity in the presence of 1 mM EDTA. *See* Specification, Table 2.

The Office alleges that it has put forth a reasonable case of inherency based simply on the fact that the presently disclosed protein and the protein of Kim are expressed in *L. starkeyi* and that their apparent molecular weights are somewhat similar. From the evidence set forth above, however, the protein of Kim is different from the protein of SEQ ID NO: 1. That is, the protein of Kim is a different enzyme of the battery of dextranases, amylases, and other glucanhydrolases secreted by *L. starkeyi*. The Office thus has not made a proper case of inherent anticipation. *See Oelrich*, 666 F.2d at 581-82. Accordingly, the rejection should be withdrawn.

Steyn *et al.*, *Gene* 166: 65-71 (Dec. 1995) ("Steyn")

Claims 1-4 and 6-10 are rejected under 35 U.S.C. § 102(b) as allegedly anticipated by Steyn *et al.*, *Gene* 166: 65-71 (Dec. 1995) ("Steyn"). Applicants traverse the rejection.

Steyn discloses a protein sequence with 88% sequence identity to SEQ ID NO: 1 and an encoding polynucleotide with 78% sequence identity to SEQ ID NO: 2. Office Action, pages 17-20. Steyn discloses neither the protein having the sequence of SEQ ID NO: 1 nor the polynucleotide having the sequence of SEQ ID NO: 2. Further, the polynucleotide of Steyn does not encode the protein of SEQ ID NO: 1. Steyn thus does not teach all the elements of the claimed invention and does not anticipate the claims. The rejection accordingly should be withdrawn.

13. Rejections under 35 U.S.C. § 103

Claim 2

Claim 2 is rejected under 35 U.S.C. § 103 as allegedly obvious over Kim in view of Standing, *Curr. Opinion Struct. Biol.* 13(5): 595-601 (2003) ("Standing") and Sambrook *et al.* **In**

MOLECULAR CLONING: A LABORATORY MANUAL, 2nd ed., Cold Spring Harbor, N.Y., pp 8.46-8.52 and 11.2-11.19 (1989) ("Sambrook"). Applicants traverse the rejection.

The Office at best makes a case that it would have been obvious for the artisan of ordinary skill to make a polynucleotide encoding the protein described in Kim. For the reasons set forth in Part 12, above, the protein of Kim is not the same as the presently disclosed protein. It follows that the polynucleotide encoding the protein of Kim cannot be the same as the claimed polynucleotide encoding the protein of SEQ ID NO: 1 or the claimed polynucleotide of SEQ ID NO: 2. The Office has not made a case that it would have been obvious to make the claimed invention, and the rejection accordingly should be withdrawn.

Claims 3, 4, and 6

Claims 3, 4, and 6 are rejected under 35 U.S.C. § 103 as allegedly obvious over Kim in view of Standing and Sambrook with respect to claim 2 and further in view of U.S. Patent No. 5,643,758 ("Guan"). Applicants traverse the rejection.

Guan does not teach the claim elements not taught by the combination of Kim, Standing and Sambrook. Guan thus does not address the deficiencies of these references, alone or in combination. The proposed combination of references thus does render the claimed invention obvious. Accordingly, the rejection should be withdrawn.

CONCLUSION

In conclusion, this amendment and reply is believed to be a full response to the outstanding Office Action. Should any issues remain outstanding or if there are any questions concerning this paper, or the application in general, the Examiner is invited to telephone the undersigned representative at the Examiner's earliest convenience.

If there are any other fees due in connection with the filing of this response, please charge the fees to our Deposit Account No. 50-0573. If a fee is required for an extension of time under 37 C.F.R. § 1.136 not accounted for above, such an extension is respectfully requested and the fee should also be charged to our Deposit Account.

Respectfully submitted,

Gwangju Do-Man KIM et al.

BY: _____

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EXHIBIT 1

BUDAPEST TREATY ON THE INTERNATIONAL RECOGNITION OF THE DEPOSIT OF MICROORGANISMS FOR THE PURPOSE OF PATENT PROCEDURE

INTERNATIONAL FORM

RECEIPT IN THE CASE OF AN ORIGINAL DEPOSIT

issued pursuant to Rule 7.1

TO : KIM, Doman
Department of Biochemical Engineering, Chungnam National University,
#220, Yongbong-dong, Puk-ku, Gwangju 500-757,
Republic of Korea

I. IDENTIFICATION OF THE MICROORGANISM	
Identification reference given by the DEPOSITOR: *Escherichia coli* DH5α/pHESA	Accession number given by the INTERNATIONAL DEPOSITARY AUTHORITY: KCTC 10573BP

II. SCIENTIFIC DESCRIPTION AND/OR PROPOSED TAXONOMIC DESIGNATION

The microorganism identified under I above was accompanied by:
[x] a scientific description
[ ] a proposed taxonomic designation
(Mark with a cross where applicable)

III. RECEIPT AND ACCEPTANCE

This International Depositary Authority accepts the microorganism identified under I above, which was received by it on **December 24 2003.**

IV. RECEIPT OF REQUEST FOR CONVERSION

The microorganism identified under I above was received by this International Depositary Authority on and a request to convert the original deposit to a deposit under the Budapest Treaty was received by it on

V. INTERNATIONAL DEPOSITARY AUTHORITY

Name: Korean Collection for Type Cultures Address: Korea Research Institute of Bioscience and Biotechnology (KRIBB) 52, Oun-dong, Yusung-ku, Taejon 305-333, Republic of Korea	Signature(s) of person(s) having the power to represent the International Depositary Authority or authorized official(s): PARK, Yong-Ha Director Date: December 30 2003

Form BP/4 (sole sheet) (cont.)